



SEQUENCE LISTING

<110> LALANNE, JEAN L
ROCHER, CORINNE

<120> Novel genes of *Candida albicans* and the proteins coded by these genes

<130> 146.1374

<140> 09/980,054

<141> 2701-11-28

<150> FR 9907250

<151> 1999-06-09

<150> PCT/FR00/01567

<151> 2000-06-08

<160> 32

<170> PatentIn Ver. 2.1

<210> 1

<211> 747

<212> DNA

<213> *Candida albicans*

<220>

<231> CDS

<232> (1)...(747)

<220>

<221> modified_base

<222> (136)...(138)

<400> 1

atg tca aat gac gat ata ata ctc cca tca gtt tca tcc tta tcg aaa 48
Met Ser Asn Asp Asp Ile Ile Leu Pro Ser Val Ser Ser Leu Ser Lys
1 5 10 15

cta act ata aat gat gta tca aaa tca gga ttt gga tac aat ccg tcc 96
Leu Thr Ile Asn Asp Val Ser Lys Ser Gly Phe Gly Tyr Asn Pro Ser
20 25 30

ata gga cca ata tca aat act att acc cta gaa tct tca ctg gta tta 144
Ile Gly Pro Ile Ser Asn Thr Ile Thr Leu Glu Ser Ser Leu Val Leu
35 40 45

tta aat aaa cgt aca ata tca tta aca cca aca tca tct gac tcc att			192
Leu Asn Lys Arg Thr Ile Ser Leu Thr Pro Thr Ser Ser Asp Ser Ile			
50	55	60	
tat gat aga aat att atc aag aaa aag cca cac gaa atc aac tta tct			240
Tyr Asp Arg Asn Ile Ile Thr Lys Lys Pro His Glu Ile Asn Leu Ser			
65	70	75	80
tcc tta tca ttt ttg ttt tgt gag att att agt tgg gca cac tct aat			288
Ser Leu Ser Phe Leu Phe Cys Glu Ile Ser Trp Ala His Ser Asn			
35	90	95	
tcc aaa ggc att caa gat tta gaa aat cgt tta aac gga tta ggt tat			336
Ser Lys Gly Ile Gln Asp Leu Glu Asn Arg Leu Asn Gly Leu Gly Tyr			
100	105	110	
caa ata ggt caa cga tat ctc gaa ttg tgt aaa ata aga gaa ggt ttt			384
Gln Ile Gly Gln Arg Tyr Leu Glu Leu Cys Lys Ile Arg Glu Gly Phe			
115	120	125	
aaa aac agt aaa cga gag att aga ctt ttg gaa atg tta caa ttt att			432
Lys Asn Ser Lys Arg Glu Ile Arg Leu Leu Glu Met Leu Gln Phe Ile			
130	135	140	
cat ggt ccg ttc tgg aaa ttg att ttt ggt aaa act gct aat gaa tta			480
His Gly Pro Phe Trp Lys Leu Ile Phe Gly Lys Thr Ala Asn Glu Leu			
145	150	155	160
gaa aaa tcg caa gat ttg ccc aat gaa tat atg att gtg gag aat gtg			528
Glu Lys Ser Gln Asp Leu Pro Asn Glu Tyr Met Ile Val Glu Asn Val			
165	170	175	
cca tta tta aat aga ttt att agt ata cct aag gag tat ggc gac tta			576
Pro Leu Leu Asn Arg Phe Ile Ser Ile Pro Lys Glu Tyr Gly Asp Leu			
180	185	190	
aat tgt tca gca ttt gtt gcg ggt ata att gag gga gca ctt gat aat			624
Asn Cys Ser Ala Phe Val Ala Gly Ile Ile Glu Gly Ala Leu Asp Asn			
195	200	205	
agt gga ttc aat gcc gat gtt aca gca cac acg gtc gct aca gat gca			672
Ser Gly Phe Asn Ala Asp Val Thr Ala His Thr Val Ala Thr Asp Ala			
210	215	220	
aat cca tta aga aca gta ttt ttg atc aag ttt gac gat tct gtt tta			720
Asn Pro Leu Arg Thr Val Phe Leu Ile Lys Phe Asp Asp Ser Val Leu			
225	230	235	240

att aga gag agt ttg aga ttt gga taa
Ile Arg Glu Ser Leu Arg Phe Gly
245

747

<210> 2
<211> 248
<1 12> PRT
<113> Candida albicans

<400> 2
Met Ser Asn Asp Asp Ile Ile Leu Pro Ser Val Ser Ser Leu Ser Lys
1 5 10 15
Leu Thr Ile Asn Asp Val Ser Lys Ser Gly Phe Gly Tyr Asn Pro Ser
20 25 30
Ile Gly Pro Ile Ser Asn Thr Ile Thr Leu Glu Ser Ser Leu Val Leu
35 40 45
Leu Asn Lys Arg Thr Ile Ser Leu Thr Pro Thr Ser Ser Asp Ser Ile
50 55 60
Tyr Asp Arg Asn Ile Ile Thr Lys Lys Pro His Glu Ile Asn Leu Ser
65 70 75 80
Ser Leu Ser Phe Leu Phe Cys Glu Ile Ile Ser Trp Ala His Ser Asn
85 90 95
Ser Lys Gly Ile Gln Asp Leu Glu Asn Arg Leu Asn Gly Leu Gly Tyr
100 105 110
Gln Ile Gly Gln Arg Tyr Leu Glu Leu Cys Lys Ile Arg Glu Gly Phe
115 120 125
Lys Asn Ser Lys Arg Glu Ile Arg Leu Leu Glu Met Leu Gln Phe Ile
130 135 140
His Gly Pro Phe Trp Lys Leu Ile Phe Gly Lys Thr Ala Asn Glu Leu
145 150 155 160
Glu Lys Ser Gln Asp Leu Pro Asn Glu Tyr Met Ile Val Glu Asn Val
165 170 175
Pro Leu Leu Asn Arg Phe Ile Ser Ile Pro Lys Glu Tyr Gly Asp Leu
180 185 190
Asn Cys Ser Ala Phe Val Ala Gly Ile Ile Glu Gly Ala Leu Asp Asn
195 200 205
Ser Gly Phe Asn Ala Asp Val Thr Ala His Thr Val Ala Thr Asp Ala
210 215 220
Asn Pro Leu Arg Thr Val Phe Leu Ile Lys Phe Asp Asp Ser Val Leu
225 230 235 240
Ile Arg Glu Ser Leu Arg Phe Gly
245

<210> 3

<211> 711
<212> DNA
<213> Candida albicans

<220>
<221> CDS
<222> (1)..(711)

<220>
<221> modified_base
<222> (577)..(579)

<400> 3
atg gat att gac gat att tta aaa gaa ttt gaa gag tct tca aaa gat 48
Met Asp Ile Asp Asp Ile Leu Lys Glu Phe Glu Glu Ser Ser Lys Asp
1 5 10 15

gaa aag att agc agt aaa aca tcg tct atc aac tta tat caa gac ttg 96
Glu Lys Ile Ser Ser Lys Thr Ser Ser Ile Asn Leu Tyr Gln Asp Leu
20 25 30

cta aga gct atg atc aac gaa cgt atg gct ccg gaa tta ttg cca tac 144
Leu Arg Ala Met Ile Asn Glu Arg Met Ala Pro Glu Leu Leu Pro Tyr
35 40 45

aaa caa gat tta atg tcc act gtt tta aca atg atg tct aac caa caa 192
Lys Gln Asp Leu Met Ser Thr Val Leu Thr Met Met Ser Asn Gln Gln
50 55 60

caa tat tta tta gaa tct cac gaa tat ggt gat atg aat ggc gac agt 240
Gln Tyr Leu Leu Glu Ser His Glu Tyr Gly Asp Met Asn Gly Asp Ser
65 70 75 80

ggg gta tta tcc gga gac ttt aaa tta caa cta atg att atc gaa act 288
Gly Val Leu Ser Gly Asp Phe Lys Leu Gln Leu Met Ile Ile Glu Thr
85 90 95

gat tta gag cgt ctc aac tat att gtt cga tta tac ata cga act cga 336
Asp Leu Glu Arg Leu Asn Tyr Ile Val Arg Leu Tyr Ile Arg Thr Arg
100 105 110

ttg agt aag ttg aat aaa ttt act att ttt tac atc aat gaa agc agt 384
Leu Ser Lys Leu Asn Lys Phe Thr Ile Phe Tyr Ile Asn Glu Ser Ser
115 120 125

caa aat gat aat tta ttg tcc aaa gag gaa aga gat tat ata cac aaa 432
Gln Asn Asp Asn Leu Leu Ser Lys Glu Glu Arg Asp Tyr Ile His Lys
130 135 140

tat ttc cag att ttg act caa tta tat aac aac tgt ttc ctc aaa aaa			480
Tyr Phe Gln Ile Leu Thr Gln Leu Tyr Asn Asn Cys Phe Leu Lys Lys			
145	150	155	160
cta cca caa atg ttg acc tat ttg gat gac acc aat ggt gga caa tca			528
Leu Pro Gln Met Leu Thr Tyr Leu Asp Asp Thr Ser Gly Gly Gln Ser			
165	170	175	
atg atc gtt gag cca gat tta gac cag cct gtg ttt atc aaa tgt acc			576
Met Ile Val Glu Pro Asp Leu Asp Gln Pro Val Phe Ile Lys Cys Thr			
180	185	190	
cug gaa gtc cca ata tta cta gat tac gac ggt gct aca gag ata gat			624
Leu Glu Val Pro Ile Leu Leu Asp Tyr Asp Gly Ala Thr Glu Ile Asp			
195	200	205	
ata gaa tta ata aaa aag gga gtc tac gtg gtg aaa tac aac cta gtc			672
Leu Glu Leu Ile Lys Lys Gly Val Tyr Val Val Lys Tyr Ser Leu Val			
210	215	220	
aaa aga tat att gat att gga gat gtg gta ttg ata tga			711
Lys Arg Tyr Ile Asp Ile Gly Asp Val Val Leu Ile			
225	230	235	

<210> 4
<211> 236
<212> PRT
<213> Candida albicans

<400> 4			
Met Asp Ile Asp Asp Ile Leu Lys Glu Phe Glu Glu Ser Ser Lys Asp			
1	5	10	15
Glu Lys Ile Ser Ser Lys Thr Ser Ser Ile Asn Leu Tyr Gln Asp Leu			
20	25	30	
Leu Arg Ala Met Ile Asn Glu Arg Met Ala Pro Glu Leu Leu Pro Tyr			
35	40	45	
Lys Gln Asp Leu Met Ser Thr Val Leu Thr Met Met Ser Asn Gln Gln			
50	55	60	
Gln Tyr Leu Leu Glu Ser His Glu Tyr Gly Asp Met Asn Gly Asp Ser			
65	70	75	80
Gly Val Leu Ser Gly Asp Phe Lys Leu Gln Leu Met Ile Ile Glu Thr			
85	90	95	
Asp Leu Glu Arg Leu Asn Tyr Ile Val Arg Leu Tyr Ile Arg Thr Arg			
100	105	110	
Leu Ser Lys Leu Asn Lys Phe Thr Ile Phe Tyr Ile Asn Glu Ser Ser			
115	120	125	

Gln	Asn	Asp	Asn	Leu	Leu	Ser	Lys	Glu	Glu	Arg	Asp	Tyr	Ile	His	Lys
130				135				140							
Tyr	Phe	Gln	Ile	Leu	Thr	Gln	Leu	Tyr	Asn	Asn	Cys	Phe	Leu	Lys	Lys
145				150				155				160			
Leu	Pro	Gln	Met	Leu	Thr	Tyr	Leu	Asp	Asp	Thr	Ser	Gly	Gly	Gln	Ser
			165				170			175					
Met	Ile	Val	Glu	Pro	Asp	Leu	Asp	Gln	Pro	Val	Phe	Ile	Lys	Cys	Thr
			180				185			190					
Leu	Glu	Val	Pro	Ile	Leu	Leu	Asp	Tyr	Asp	Gly	Ala	Thr	Glu	Ile	Asp
			195				200			205					
Leu	Glu	Leu	Ile	Lys	Lys	Gly	Val	Tyr	Val	Val	Lys	Tyr	Ser	Leu	Val
			210				215			220					
Lys	Arg	Tyr	Ile	Asp	Ile	Gly	Asp	Val	Val	Leu	Ile				
			225				230			235					

<310> 5

<311> 1383

<312> DNA

<313> Candida albicans

<320>

<321> CDS

<322> (1)...(1383)

<400> 5

atg	gat	tcc	ata	gga	gag	att	ata	gag	cat	gag	aca	gag	gca	cct	aaa
Met	Asp	Phe	Ile	Gly	Glu	Ile	Ile	Glu	His	Glu	Thr	Glu	Ala	Pro	Lys
1				5				10							48

gaa	cca	acc	cca	aaa	ccc	aca	att	ggc	gga	tcc	ccc	gaa	ctt	aaa	aaa
Glu	Pro	Thr	Pro	Lys	Pro	Thr	Ile	Gly	Gly	Phe	Pro	Glu	Leu	Lys	Lys
				20				25							96

tta	aaa	gaa	aag	aaa	gtc	tca	aga	tgg	agg	caa	aag	caa	caa	cag	gaa
Leu	Lys	Glu	Lys	Val	Ser	Arg	Trp	Arg	Gln	Gln	Gln	Gln	Glu		144
				35			40			45					

cag	agc	aca	act	tcc	cca	aaa	act	act	gaa	atc	cgt	tca	gag	gct	tcc
Gln	Ser	Thr	Thr	Ser	Pro	Lys	Thr	Thr	Glu	Ile	Arg	Ser	Glu	Ala	Ser
				50				55		60					192

aaa	att	cac	caa	gaa	aat	atc	gag	aag	atg	gct	caa	atg	tca	gag	gaa
Lys	Ile	His	Gln	Glu	Asn	Ile	Glu	Lys	Met	Ala	Gln	Met	Ser	Glu	Glu
				65			70		75			80			240

gag	att	tgc	caa	gag	cgt	gag	gag	tta	aag	ggt	tta	gat	cct	aaa
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Glu	Ile	Leu	Gln	Glu	Arg	Glu	Glu	Leu	Leu	Lys	Gly	Leu	Asp	Pro	Lys	
85								90					95			
tta	att	gaa	agt	ttg	att	ggg	aga	tcc	aag	aaa	agg	gaa	gca	aca	gac	336
Leu	Ile	Glu	Ser	Ile	Ile	Gly	Arg	Ser	Lys	Lys	Arg	Glu	Ala	Thr	Asp	
100								105					110			
cat	gaa	cac	aat	gga	cat	gtc	cat	gaa	cat	gca	gag	gga	tac	cat	gga	384
His	Glu	His	Asn	Gly	His	Ala	His	Glu	His	Ala	Glu	Gly	Tyr	His	Gly	
115								120					125			
tgg	att	gga	tca	atg	aaa	act	tct	gaa	gga	tta	aca	gat	tta	tct	caa	432
Trp	Ile	Gly	Ser	Met	Lys	Thr	Ser	Glu	Gly	Leu	Thr	Asp	Leu	Ser	Gln	
130								135					140			
tta	gat	aag	gaa	gat	gtg	gac	cg	gca	ttg	gg	ata	agt	tca	tta	tcc	480
Leu	Asp	Lys	Glu	Asp	Val	Asp	Arg	Ala	Leu	Gly	Ile	Ser	Ser	Leu	Ser	
145								150					155			160
tta	tct	gaa	cct	gag	gg	gg	ag	gac	aaa	aaa	gtc	gct	tcc	gac		528
Leu	Ser	Glu	Pro	Glu	Gly	Gly	Ser	Asn	Thr	Lys	Lys	Val	Ala	Phe	Asp	
165								170					175			
gat	aat	atc	aag	acg	gtt	aaa	ttt	gaa	gat	ttg	gat	gat	gga	att	gaa	576
Asp	Asn	Ile	Lys	Thr	Val	Lys	Phe	Glu	Asp	Leu	Asp	Asp	Gly	Ile	Glu	
180								185					190			
ttg	gat	cca	aat	gga	ttg	gag	gac	gtt	act	gat	gtc	aat	gaa	tta	gtt	604
Leu	Asp	Pro	Asn	Gly	Trp	Glu	Asp	Val	Thr	Asp	Val	Asn	Glu	Leu	Val	
195								200					205			
cct	aat	aat	gat	caa	att	gca	cct	gac	gat	tac	cag	att	aat	cct	gat	672
Pro	Asn	Asn	Asp	His	Ile	Ala	Pro	Asp	Asp	Tyr	Gln	Ile	Asn	Pro	Asp	
210								215					220			
agc	gat	gaa	gaa	gga	ttg	aat	aat	act	gtt	cat	ttt	aca	aaa	ccc	aaa	720
Ser	Asp	Glu	Glu	Gly	Leu	Asn	Asn	Thr	Val	His	Phe	Thr	Lys	Pro	Lys	
225								230					235			240
cag	cca	gat	ttg	gat	ata	aat	gat	cct	ttt	gat	aag	cta	cat			768
Gln	Pro	Asp	Leu	Asp	Ile	Asn	Asp	Pro	Asp	Phe	Phe	Asp	Lys	Leu	His	
245								250					255			
gag	aaa	tac	tat	cct	gat	ttg	cct	aaa	gaa	aca	gaa	aag	ttg	tca	tgg	816
Glu	Lys	Tyr	Tyr	Pro	Asp	Leu	Pro	Lys	Glu	Thr	Glu	Lys	Leu	Ser	Trp	
260								265					270			
atg	aca	cac	ttt	atg	cca	aaa	caa	ttg	tct	acc	gtt	tat	gaa	tca	ata	864

Met Thr Gln Pro Met Pro Lys Gln Leu Ser Thr Val Tyr Glu Ser Ile				
275	280	285		
tct gat atg aga ttt gac tti aaa gga gat tta att gaa ttg ggt cca				912
Ser Asp Met Arg Phe Asp Phe Lys Gly Asp Leu Ile Glu Leu Gly Pro				
290	295	300		
gag gga gaa gaa cca aaa gat agt tca tcc gaa ata cct act tat atg				960
Glu Gly Glu Glu Pro Lys Asp Ser Ser Glu Ile Pro Thr Tyr Met				
305	310	315	320	
gga ctt cat tat cat tcg gag aac cca cat atg gca ggt tat aca ttg				1008
Gly Leu His His Ser Glu Asn Pro His Met Ala Gly Tyr Thr Leu				
325	330	335		
ggt gag ttg gca cat tta gct aga tcg act tta gct gga caa aga tgc				1056
Gly Glu Leu Ala His Leu Ala Arg Ser Thr Leu Ala Gly Gln Arg Cys				
340	345	350		
ttg agc att caa aca tta ggg aga atc tta cat aaa ttg gga tta cat				1104
Leu Ser Ile Gln Thr Leu Gly Arg Ile Leu His Lys Leu Gly Leu His				
355	360	365		
aaa tac agt ata cta cca aaa aca gac tca gat gat cag agt ttt aca				1152
Lys Tyr Ser Ile Leu Pro Lys Thr Asp Ser Asp Asp Gln Ser Phe Thr				
370	375	380		
gat gaa atc aaa caa cta tca ctt gag ttt gaa gat atg atg tgg jac				1200
Asp Glu Ile Lys Gln Leu Ser Leu Asp Phe Glu Asp Met Met Trp Asp				
385	390	395	400	
ttg ata gac caa tta cga atc att gaa aca ata aca gag gca gct gat				1248
Leu Ile Asp Gln Leu Arg Ile Ile Glu Thr Ile Thr Glu Ala Ala Asp				
405	410	415		
gaa aaa aag acc aga aac tta tot gtc aga aat tat gca ata gag gca				1296
Glu Lys Lys Thr Arg Asn Leu Ser Val Arg Asn Tyr Ala Ile Glu Ala				
420	425	430		
ttg tgg tta tat aga act gga ggt gga aga cca gag ata act aaa caa				1344
Leu Trp Leu Tyr Arg Thr Gly Gly Arg Pro Glu Ile Thr Lys Gln				
435	440	445		
acc gaa gag gat ttg ata gca caa gca gtt sag aaa taa				1383
Thr Glu Glu Asp Leu Ile Ala Gln Ala Val Gln Lys				
450	455	460		

<210> 6
<211> 460
<212> PRT
<213> Candida albicans

<400> 6
Met Asp Phe Ile Gly Glu Ile Ile Glu His Glu Thr Glu Ala Pro Lys
1 5 10 15
Glu Pro Thr Pro Lys Pro Thr Ile Gly Gly Phe Pro Glu Leu Lys Lys
20 25 30
Leu Lys Glu Lys Lys Val Ser Arg Trp Arg Gln Lys Gln Gln Glu
35 40 45
Gln Ser Thr Thr Ser Pro Lys Thr Thr Glu Ile Arg Ser Glu Ala Ser
50 55 60
Lys Ile His Gln Glu Asn Ile Glu Lys Met Ala Gln Met Ser Glu Glu
65 70 75 80
Glu Ile Leu Gln Glu Arg Glu Glu Leu Leu Lys Gly Leu Asp Pro Lys
85 90 95
Leu Ile Glu Ser Leu Ile Gly Arg Ser Lys Lys Arg Glu Ala Thr Asp
100 105 110
His Glu His Asn Gly His Ala His Glu His Ala Glu Gly Tyr His Gly
115 120 125
Trp Ile Gly Ser Met Lys Thr Ser Glu Gly Leu Thr Asp Leu Ser Gln
130 135 140
Leu Asp Lys Glu Asp Val Asp Arg Ala Leu Gly Ile Ser Ser Leu Ser
145 150 155 160
Leu Ser Glu Pro Glu Gly Gly Ser Asn Thr Lys Lys Val Ala Phe Asp
165 170 175
Asp Asn Ile Lys Thr Val Lys Phe Glu Asp Leu Asp Asp Gly Ile Glu
180 185 190
Leu Asp Pro Asn Gly Trp Glu Asp Val Thr Asp Val Asn Glu Leu Val
195 200 205
Pro Asn Asn Asp His Ile Ala Pro Asp Asp Tyr Gln Ile Asn Pro Asp
210 215 220
Ser Asp Glu Glu Gly Leu Asn Asn Thr Val His Phe Thr Lys Pro Lys
225 230 235 240
Gln Pro Asp Leu Asp Ile Asn Asp Pro Asp Phe Phe Asp Lys Leu His
245 250 255
Glu Lys Tyr Tyr Pro Asp Leu Pro Lys Glu Thr Glu Lys Leu Ser Trp
260 265 270
Met Thr Gln Pro Met Pro Lys Gln Leu Ser Thr Val Tyr Glu Ser Ile
275 280 285
Ser Asp Met Arg Phe Asp Phe Lys Gly Asp Leu Ile Glu Leu Gly Pro
290 295 300
Glu Gly Glu Glu Pro Lys Asp Ser Ser Ser Glu Ile Pro Thr Tyr Met
305 310 315 320
Gly Leu His His Ser Glu Asn Pro His Met Ala Gly Tyr Thr Leu
325 330 335

Gly Glu Leu Ala His Leu Ala Arg Ser Thr Leu Ala Gly Gln Arg Cys
 340 345 350
 Leu Ser Ile Gln Thr Leu Gly Arg Ile Leu His Lys Leu Gly Leu His
 355 360 365
 Lys Tyr Ser Ile Leu Pro Lys Thr Asp Ser Asp Asp Gln Ser Phe Thr
 370 375 380
 Asp Glu Ile Lys Gln Leu Ser Leu Asp Phe Glu Asp Met Met Trp Asp
 385 390 395 400
 Leu Ile Asp Gln Leu Arg Ile Ile Glu Thr Ile Thr Glu Ala Ala Asp
 405 410 415
 Glu Lys Lys Thr Arg Asn Leu Ser Val Arg Asn Tyr Ala Ile Glu Ala
 420 425 430
 Leu Trp Leu Tyr Arg Thr Gly Gly Arg Pro Glu Ile Thr Lys Gln
 435 440 445
 Thr Glu Glu Asp Leu Ile Ala Gln Ala Val Gln Lys
 450 455 460

<210> 7
 <211> 1383
 <212> DNA
 <213> Candida albicans

<220>
 <221> CDS
 <222> (1)...(1380)

<400> 7
 atg gat ttc ata gga gag att ata gag cat gag aca gag gca cct aaa 48
 Met Asp Phe Ile Gly Glu Ile Ile Glu His Glu Thr Glu Ala Pro Lys
 1 5 10 15

 gaa cca acc cca aaa ccc aca att ggt gga ttc ccc gaa ctt aaa aaa 96
 Glu Pro Thr Pro Lys Pro Thr Ile Gly Gly Phe Pro Glu Leu Lys Lys
 20 25 30

 tta aaa gaa aag aaa gtc tca aga tgg agg caa aag caa caa cag gag 144
 Leu Lys Glu Lys Lys Val Ser Arg Trp Arg Gln Lys Gln Gln Glu
 35 40 45

 cag aag aca act tcc cca aaa act act gaa atc cgt tca gag gct tcc 192
 Gln Ser Thr Thr Ser Pro Lys Thr Thr Glu Ile Arg Ser Glu Ala Ser
 50 55 60

 aia att cac caa gaa aat atc gag aag atg gct caa atg tca gag gaa 240
 Lys Ile His Gln Glu Asn Ile Gln Lys Met Ala Gln Met Ser Glu Glu
 65 70 75 80

gag att ttg caa gag cgt gag gag tta cta aag ggt tta gac cct aaa Glu Ile Leu Gln Glu Arg Glu Glu Leu Leu Lys Gly Leu Asp Pro Lys	85	90	95	283
tta att gaa agt ttg att ggt aga tcc aag aaa agg gaa gca aca gac Leu Ile Glu Ser Leu Ile Gly Arg Ser Lys Lys Arg Glu Ala Thr Asp	100	105	110	336
cat gaa cac aat gga cat gct cat gaa cat gca gag gga tac cat gga His Glu His Asn Gly His Ala His Glu His Ala Glu Gly Tyr His Gly	115	120	125	384
tgg att gga tca atg aaa act tct gaa gga tta aca gat tta tct caa Trp Ile Gly Ser Met Lys Thr Ser Glu Gly Leu Thr Asp Leu Ser Gln	130	135	140	430
tta gat aag gaa gat gtg gac cgt gct ttg ggt ata agt tca tta tcc Leu Asp Lys Glu Asp Val Asp Arg Ala Leu Gly Ile Ser Ser Leu Ser	145	150	155	480
tta tct gaa cct gag ggt ggc agc aat acg aaa aaa gtc gct ttc gac Leu Ser Glu Pro Glu Gly Ser Asn Thr Lys Lys Val Ala Phe Asp	165	170	175	528
gat aat atc aag acg gtt aaa ttt gaa gct ttg gat gat gaa att gaa Asp Asn Ile Lys Thr Val Lys Phe Glu Ala Leu Asp Asp Glu Ile Glu	180	185	190	576
ttg gat cca aat gga tgg gag gac gtt act gat gtc aat gaa tta gtt Leu Asp Pro Asn Gly Trp Glu Asp Val Thr Asp Val Asn Glu Leu Val	195	200	205	624
cct aat aat gat cac att gca cct gac gat tac cag att aat cct gat Pro Asn Asn Asp His Ile Ala Pro Asp Asp Tyr Gln Ile Asn Pro Asp	210	215	220	671
agc gat gaa gaa gga ttg aat aat act gtt cat ttt aca aaa ccc aaa Ser Asp Glu Glu Gly Leu Asn Asn Thr Val His Phe Thr Lys Pro Lys	225	230	235	720
cag cca gat ttg gat ata aat gat ccc gat ttc ttt gat aag cta cat Gln Pro Asp Leu Asp Ile Asn Asp Pro Asp Phe Phe Asp Lys Leu His	245	250	255	769
aaag aaa tat tat cct gat ttg cct aaa gaa aca gaa aag ttg tca tgg Glu Lys Tyr Tyr Pro Asp Leu Pro Lys Glu Thr Glu Lys Leu Ser Trp	260	265	270	816

atg aca ccc atg cca aaa caa ttg tct aca gtt tat gaa tca ata 864
Met Thr Gln Pro Met Pro Lys Gln Leu Ser Thr Val Tyr Glu Ser Ile
275 280 285

tct gat atg aga ttt gac ttc aaa gga gat tta att gaa ttg agc gca 912
Ser Asp Met Arg Phe Asp Phe Lys Gly Asp Leu Ile Glu Leu Ser Ala
290 295 300

gag gga gaa gaa cca aaa gat aat tca ttc gaa ata cct act tat atg 960
Glu Gly Glu Glu Pro Lys Asp Ser Ser Phe Glu Ile Pro Thr Tyr Met
305 310 315 320

gga ctt cat cat cat tcg gag aac cca cat atg gca ggt tat aca ttg 1008
Gly Leu His His His Ser Glu Asn Pro His Met Ala Gly Tyr Thr Leu
325 330 335

ggc gag ttc gca cat tta gcc aga tcg act tta gct gga caa aga tgc 1056
Gly Glu Leu Ala His Leu Ala Arg Ser Thr Leu Ala Gly Gln Arg Cys
340 345 350

ttg aac att caa aca tta ggg aga ata tta cat aaa ttg gga tta cat 1104
Leu Ser Ile Gln Thr Leu Gly Arg Ile Leu His Lys Leu Gly Leu His
355 360 365

aaa tac aat ata cta cca aaa aca gac tca gat gat cag aat ttt aca 1152
Lys Tyr Ser Ile Leu Pro Lys Thr Asp Ser Asp Asp Gln Ser Phe Thr
370 375 380

gat gaa atc aaa caa cta tca ctt gac ttt gaa gat atg atg tgg gac 1200
Asp Glu Ile Lys Gln Leu Ser Leu Asp Phe Glu Asp Met Met Trp Asp
385 390 395 400

ttg ata gac caa tta cga atc att gaa aca ata aca gag gca gct gat 1243
Leu Ile Asp Gln Leu Arg Ile Ile Glu Thr Ile Thr Glu Ala Ala Asp
405 410 415

gaa aaa aag acc aga aac tta tct gtc aga aat tat gca ata gag gca 1296
Glu Lys Lys Thr Arg Asn Leu Ser Val Arg Asn Tyr Ala Ile Glu Ala
420 425 430

ttg tgg tta tat aga act gga ggt gga aga cca gag ata act aaa caa 1344
Leu Trp Leu Tyr Arg Thr Gly Gly Arg Pro Glu Ile Thr Lys Gln
435 440 445

acc gaa gag gat ttg ata gca caa gca gtt cag aaa taa 1383
Thr Glu Glu Asp Leu Ile Ala Gln Ala Val Gln Lys
450 455 460

<210> 8
<211> 460
<212> PRT
<213> Candida albicans

<400> 9
Met Asp Phe Ile Gly Glu Ile Ile Glu His Glu Thr Glu Ala Pro Lys
1 5 10 15

Glu Pro Thr Pro Lys Pro Thr Ile Gly Gly Phe Pro Glu Leu Lys Lys
20 25 30

Leu Lys Glu Lys Lys Val Ser Arg Trp Arg Gln Lys Gln Gln Glu
35 40 45

Gln Ser Thr Thr Ser Pro Lys Thr Thr Glu Ile Arg Ser Glu Ala Ser
50 55 60

Lys Ile His Gln Glu Asn Ile Glu Lys Met Ala Gln Met Ser Glu Glu
65 70 75 80

Glu Ile Leu Gln Glu Arg Glu Glu Leu Leu Lys Gly Leu Asp Pro Lys
85 90 95

Leu Ile Glu Ser Leu Ile Gly Arg Ser Lys Lys Arg Glu Ala Thr Asp
100 105 110

His Glu His Asn Gly His Ala His Glu His Ala Glu Gly Tyr His Gly
115 120 125

Trp Ile Gly Ser Met Lys Thr Ser Glu Gly Leu Thr Asp Leu Ser Gln
130 135 140

Leu Asp Lys Glu Asp Val Asp Arg Ala Leu Gly Ile Ser Ser Leu Ser
145 150 155 160

Leu Ser Glu Pro Glu Gly Gly Ser Asn Thr Lys Lys Val Ala Phe Asp
165 170 175

Asp Asn Ile Lys Thr Val Lys Phe Glu Ala Leu Asp Asp Glu Ile Glu
180 185 190

Leu Asp Pro Asn Gly Trp Glu Asp Val Thr Asp Val Asn Glu Leu Val
195 200 205

Pro Asn Asn Asp His Ile Ala Pro Asp Asp Tyr Gln Ile Asn Pro Asp

210 215 220
Ser Asp Glu Glu Gly Leu Asn Asn Thr Val His Phe Thr Lys Pro Lys
225 230 235 240

Gln Pro Asp Leu Asp Ile Asn Asp Pro Asp Phe Phe Asp Lys Leu His
245 250 255

Glu Lys Tyr Tyr Pro Asp Leu Pro Lys Glu Thr Glu Lys Leu Ser Trp
260 265 270

Met Thr Gln Pro Met Pro Lys Gln Leu Ser Thr Val Tyr Glu Ser Ile
275 280 285

Ser Asp Met Arg Phe Asp Phe Lys Gly Asp Leu Ile Glu Leu Ser Ala
290 295 300

Glu Gly Glu Glu Pro Lys Asp Ser Ser Phe Glu Ile Pro Thr Tyr Met
305 310 315 320

Gly Leu His His Ser Glu Asn Pro His Met Ala Gly Tyr Thr Leu
325 330 335

Gly Glu Leu Ala His Leu Ala Arg Ser Thr Leu Ala Gly Gln Arg Cys
340 345 350

Leu Ser Ile Gln Thr Leu Gly Arg Ile Leu His Lys Leu Gly Leu His
355 360 365

Lys Tyr Ser Ile Leu Pro Lys Thr Asp Ser Asp Asp Gln Ser Phe Thr
370 375 380

Asp Glu Ile Lys Gln Leu Ser Leu Asp Phe Glu Asp Met Met Trp Asp
385 390 395 400

Leu Ile Asp Gln Leu Arg Ile Ile Glu Thr Ile Thr Glu Ala Ala Asp
405 410 415

Glu Lys Lys Thr Arg Asn Leu Ser Val Arg Asn Tyr Ala Ile Glu Ala
420 425 430

Leu Trp Leu Tyr Arg Thr Gly Gly Arg Pro Glu Ile Thr Lys Gln
435 440 445

Thr Glu Glu Asp Leu Ile Ala Gln Ala Val Gln Lys
450 455 460

<210> 9
 <211> 2262
 <212> DNA
 <213> Candida albicans

 <220>
 <221> CDS
 <222> (1)..(2262)

 <230>
 <231> modified_base
 <232> (1093)..(1095)

 <240>
 <241> modified_base
 <242> (1828)..(1830)

 <400> 9
 atg gca gca gca cca cca cca gcg aaa aac cag ggt aag gca aaa 48
 Met Ala Ala Ala Pro Pro Pro Ala Lys Asn Gln Gly Lys Ala Lys
 1 5 10 15

 cag cat gtt aca ggt gcc agg ttc cgt cag cga aaa atc tcg gta aag 96
 Gln His Val Thr Gly Ala Arg Phe Arg Gln Arg Lys Ile Ser Val Lys
 20 25 30

 cag ccc ttg act att tat aaa cag aga gac cta cct act cta gat agc 144
 Gln Pro Leu Thr Ile Tyr Lys Gln Arg Asp Leu Pro Thr Leu Asp Ser
 35 40 45

 aat gag tta gag cct agtcaa gtc cat cat tta aat tct aat gcg tca 192
 Asn Glu Leu Glu Pro Ser Gln Val His His Leu Asn Ser Asn Ala Ser
 50 55 60

 tca tca tca aca caa caa ccg aga gac ctt cat gca gtt gaa act ggg 240
 Ser Ser Ser Thr Gln Gln Pro Arg Asp Leu His Ala Val Glu Thr Gly
 65 70 75 80

 gtt gag aat gag gaa gag gaa gtg cat ctt cag caa gtt atc aat 288
 Val Asp Asn Glu Glu Glu Val His Leu Gln Gln Val Ile Asn
 85 90 95

 gct gca caa aaa gca ctt ttg ggt tcg aaa aaa gaa gaa aaa agc agt 336
 Ala Ala Gln Lys Ala Leu Leu Gly Ser Lys Lys Glu Glu Lys Ser Ser
 100 105 110

 gat atg tat att ccc aca ccg gac gct tcg agg ata tgg ccc gag gca 384

Asp Met Tyr Ile Pro Thr Pro Asp Ala Ser Arg Ile Trp Pro Glu Ala			
115	120	125	
cac aag tat tac aag gat caa aag ttc aag cag cca gag aca tat atc			432
His Lys Tyr Tyr Lys Asp Gln Lys Phe Lys Gln Pro Glu Thr Tyr Ile			
130	135	140	
aag ttt agt gcg aca gta gag gac aca gtc ggt gtc gag tac aat atg			480
Lys Phe Ser Ala Thr Val Glu Asp Thr Val Gly Val Glu Tyr Asn Met			
145	150	155	160
gac gag gta gat gaa aag ttt tat aga gag aca cta tgc aag tac tat			528
Asp Glu Val Asp Glu Lys Phe Tyr Arg Glu Thr Leu Cys Lys Tyr Tyr			
165	170	175	
ccc aaa aag aaa aac aag tca gat gag aac aat cga aag tgt act gaa			576
Pro Lys Lys Lys Asn Lys Ser Asp Glu Asn Asn Arg Lys Cys Thr Glu			
180	185	190	
tgg gag ttt gaa aca atc tgt gac aag ttg gaa aag acc att gaa gca			624
Leu Glu Phe Glu Thr Ile Cys Asp Lys Leu Glu Lys Thr Ile Glu Ala			
195	200	205	
cga caa ccg ttt ttg tct atg gac ccc agc aac att cta tcg tac gag			672
Arg Gln Pro Phe Leu Ser Met Asp Pro Ser Asn Ile Leu Ser Tyr Glu			
210	215	220	
gag ttg tcg tcg tac att gtc gat cag ttt aaa agt gca gtc aaa aca			720
Glu Leu Ser Ser Tyr Ile Val Asp Gln Phe Lys Ser Ala Val Lys Thr			
225	230	235	240
agc aac ccg tat att gtt acc aat ggt ggg aat cta gag tat aia tcg			768
Ser Asn Pro Tyr Ile Val Thr Asn Gly Gly Asn Leu Glu Tyr Ile Ser			
245	250	255	
acg aca gct tta aaa gag aga ttg tcg aag gaa ata aag tat gaa ccg			816
Thr Thr Ala Leu Lys Glu Arg Leu Ser Lys Glu Ile Lys Tyr Glu Pro			
260	265	270	
ttt gtt act att ttt gat aag aac caa atg tcc aca agt gcg gtc aga			864
Phe Val Thr Ile Phe Asp Lys Asn Gln Met Ser Thr Ser Ala Val Arg			
275	280	285	
ttt att ccc aaa ttg ttt gag tcg ttg ggc aga ctt gtt tat gat cat			912
Pro Ile Pro Lys Leu Phe Glu Ile Phe Gly Arg Pro Val Tyr Asp His			
290	295	300	
tgg aag gag aga aaa ata gaa aga aag ggc aaa acc atc cag ccc aca			960

Trp Lys Glu Arg Lys Ile Glu Arg Lys Gly Lys Thr Ile Gln Pro Thr				
305	310	315	320	
ctt aaa ttt gag gat cct aac tcg aac gaa aag gaa aac gac aat gac				1008
Leu Lys Phe Glu Asp Pro Asn Ser Asn Glu Lys Glu Asn Asp Asn Asp				
325	330	335		
cca tat ata tgt ttc aga cga cgt gag ttt agg caa gca aga aag acg				1056
Pro Tyr Ile Cys Phe Arg Arg Glu Phe Arg Gln Ala Arg Lys Thr				
340	345	350		
aga aga gcc gat aca att ggt gca gag aga ata aga ctg atg caa aag				1104
Arg Arg Ala Asp Thr Ile Gly Ala Glu Arg Ile Arg Leu Met Gln Lys				
355	360	365		
tcg ttg cac cgc gca cgt gat ttg ata atg agt gtt agt gaa aga gag				1152
Ser Leu His Arg Ala Arg Asp Leu Ile Met Ser Val Ser Glu Arg Glu				
370	375	380		
atc ctc aaa ctc gac aat ttt caa gca gag cat gaa ttg ttt aaa gcc				1200
Ile Leu Lys Leu Asp Asn Phe Gln Ala Glu Leu Phe Lys Ala				
385	390	395	400	
agg tgc gct acc aag gct tgt aag agg gag ctc aat atc aag ggt gac				1248
Arg Cys Ala Thr Lys Ala Cys Lys Arg Glu Leu Asn Ile Lys Gly Asp				
405	410	415		
gaa tac ttg ttc ttt ccg cat aaa aag aag aaa att gtt cgt act gaa				1296
Glu Tyr Leu Phe Phe Pro His Lys Lys Lys Ile Val Arg Thr Glu				
420	425	430		
gat gaa gaa agg gag aag aag aga gaa aag aag aag caa gac caa gaa				1344
Asp Glu Glu Arg Glu Lys Lys Arg Glu Lys Lys Gln Asp Gln Glu				
435	440	445		
ctt gca ctc aag caa caa gca cta cag caa cag cag caa cca cca				1392
Leu Ala Leu Lys Gln Gln Ala Leu Gln Gln Gln Gln Gln Pro				
450	455	460		
cca caa cca cca caa gca cca tca aaa caa gat ggt aca tca acg				1440
Pro Gln Pro Pro Gln Gln Ala Pro Ser Lys Gln Asp Gly Thr Ser Thr				
465	470	475	480	
agc cag cct tat gtc aaa ctc cca ccc gca aaa gtt cca gat atg gat				1488
Ser Gln Pro Tyr Val Lys Leu Pro Pro Ala Lys Val Pro Asp Met Asp				
485	490	495		
ctt gtt aca gtt tcg ttg gta tta aag gaa aag aac gaa acc atc aaa				1536

Leu Val Thr Val Ser Leu Val Leu Lys Glu Lys Asn Glu Thr Ile Lys			
500	505	510	
cgt gct gtg ttg gag aaa ttg cgc aag aga aag gaa cac gac aag gga			1584
Arg Ala Val Leu Glu Lys Leu Arg Lys Arg Lys Glu His Asp Lys Gly			
515	520	525	
ttt atc aat ttt aca gac gat tcg tat cag cca ttt ttc gat att tca			1632
Phe Ile Asn Leu Thr Asp Asp Pro Tyr Gln Pro Phe Phe Asp Ile Ser			
530	535	540	
acc aat agg gcc gaa gag ttg agc cat att ccg tat tcg tcg att gcc			1680
Thr Asn Arg Ala Glu Glu Leu Ser His Ile Pro Tyr Ser Ser Ile Ala			
545	550	555	560
gcc aca cac tat cac caa ttc aac aca tcg aac tac atg aac gac caa			1728
Ala Thr His Tyr His Gln Phe Asn Thr Ser Asn Tyr Met Asn Asp Gln			
565	570	575	
ctt aaa aag cta ctt gaa gag aaa aaa cct tta cct ggt gta aaa acg			1776
Leu Lys Lys Leu Leu Glu Glu Lys Lys Pro Leu Pro Gly Val Lys Thr			
580	585	590	
ttt ttg ggt tat aac ggg gag ttg gta cca tcg aag gca ttt cca cat			1824
Phe Leu Gly Ser Asn Gly Glu Leu Val Pro Ser Lys Ala Phe Pro His			
595	600	605	
ttg ctg tcg tcg ctt gag gaa aag tat aag gcc aca agt ggg tat att			1872
Leu Leu Ser Leu Leu Glu Glu Lys Tyr Lys Ala Thr Ser Gly Tyr Ile			
610	615	620	
gaa cga tta ttg caa agc gtg gag acg caa gat ttt agt tca tac acc			1920
Glu Arg Leu Leu Gln Ser Val Glu Thr Gln Asp Phe Ser Ser Tyr Thr			
625	630	635	640
aat ggc ttt aaa gat gtt gag cca aaa gaa aca aat gaa cct gtt atg			1968
Asn Gly Phe Lys Asp Val Glu Pro Lys Glu Thr Asn Glu Pro Val Met			
645	650	655	
ggc ttt ccc caa aga ata cgt cga aca gtg ggc agg gct ggc agg gtt			2016
Ala Phe Pro Gln Arg Ile Arg Arg Val Gly Arg Ala Gly Arg Val			
660	665	670	
ttt ttg gac cac cag caa gag tac ccg caa ccg aat ttt cag caa gac			2064
Phe Leu Asp His Gln Gln Glu Tyr Pro Gln Pro Asn Phe Gln Gln Asp			
675	680	685	
aca cat cgt gtg gga ggt atc cca gat gtg tat tgt aaa gag gat gcc			2112

Thr Asp Arg Val Gly Gly Ile Pro Asp Val Tyr Cys Lys Glu Asp Ala			
690	695	700	
att aaa cga tta cag tca aag tgg aag ttc gat aca gaa tat aaa aca			2160
Ile Lys Arg Leu Gln Ser Lys Trp Lys Phe Asp Thr Glu Tyr Lys Thr			
705	710	715	720
act gaa cca ttt agt ttg gat cct tca aag ttg aat ggt att agt cca			2208
Thr Glu Pro Phe Ser Leu Asp Pro Ser Lys Leu Asn Gly Ile Ser Pro			
725	730	735	
ttt aac caa tcg att aga tti ggg tct atg ttg ttg aat aqa aca ctt			2256
Ser Thr Gln Ser Ile Arg Phe Gly Ser Met Leu Leu Asn Arg Thr Arg			
740	745	750	
aaa tag			2262
Lys			

<210> 10
<211> 753
<212> PRT
<213> Candida albicans

<400> 10			
Met Ala Ala Ala Pro Pro Pro Pro Ala Lys Asn Gln Gly Lys Ala Lys			
1	5	10	15
Gln His Val Thr Gly Ala Arg Phe Arg Gln Arg Lys Ile Ser Val Lys			
20	25	30	
Gln Pro Leu Thr Ile Tyr Lys Gln Arg Asp Leu Pro Thr Leu Asp Ser			
35	40	45	
Asn Glu Leu Glu Pro Ser Gln Val His His Leu Asn Ser Asn Ala Ser			
50	55	60	
Ser Ser Ser Thr Gln Gln Pro Arg Asp Leu His Ala Val Glu Thr Gly			
65	70	75	80
Val Asp Lys Asn Gln Glu Glu Glu Val His Leu Gln Gln Val Ile Asn			
85	90	95	
Ala Ala Gln Lys Ala Leu Leu Gly Ser Lys Lys Glu Glu Lys Ser Ser			
100	105	110	
Asp Met Tyr Ile Pro Thr Pro Asp Ala Ser Arg Ile Trp Pro Glu Ala			
115	120	125	
His Lys Tyr Tyr Lys Asp Gln Lys Phe Lys Gln Pro Glu Thr Tyr Ile			
130	135	140	
Lys Phe Ser Ala Thr Val Glu Asp Thr Val Gly Val Glu Tyr Asn Met			
145	150	155	160
Asp Glu Val Asp Glu Lys Phe Tyr Arg Glu Thr Leu Cys Lys Tyr Tyr			
165	170	175	
Pro Lys Lys Lys Asn Lys Ser Asp Glu Asn Asn Arg Lys Cys Thr Glu			

180	185	190
Leu Glu Phe Glu Thr Ile Cys Asp Lys Leu Glu Lys Thr Ile Glu Ala		
195	200	205
Arg Gln Pro Phe Leu Ser Met Asp Pro Ser Asn Ile Leu Ser Tyr Glu		
210	215	220
Glu Leu Ser Ser Tyr Ile Val Asp Gln Phe Lys Ser Ala Val Lys Thr		
225	230	235
Ser Asn Pro Tyr Ile Val Thr Asn Gly Gly Asn Leu Glu Tyr Ile Ser		
245	250	255
Thr Thr Ala Leu Lys Glu Arg Leu Ser Lys Glu Ile Lys Tyr Glu Pro		
260	265	270
Phe Val Thr Ile Phe Asp Lys Asn Gln Met Ser Thr Ser Ala Val Arg		
275	280	285
Pro Ile Pro Lys Leu Phe Glu Leu Phe Gly Arg Pro Val Tyr Asp His		
290	295	300
Trp Lys Glu Arg Lys Ile Glu Arg Lys Gly Lys Thr Ile Gln Pro Thr		
305	310	315
Leu Lys Phe Glu Asp Pro Asn Ser Asn Glu Lys Glu Asn Asp Asn Asp		
325	330	335
Pro Tyr Ile Cys Phe Arg Arg Arg Glu Phe Arg Gln Ala Arg Lys Thr		
340	345	350
Arg Arg Ala Asp Thr Ile Gly Ala Glu Arg Ile Arg Leu Met Gln Lys		
355	360	365
Ser Leu His Arg Ala Arg Asp Leu Ile Met Ser Val Ser Glu Arg Glu		
370	375	380
Ile Leu Lys Leu Asp Asn Phe Gln Ala Glu His Glu Leu Phe Lys Ala		
385	390	395
Arg Cys Ala Thr Lys Ala Cys Lys Arg Glu Leu Asn Ile Lys Gly Asp		
405	410	415
Glu Tyr Leu Phe Phe Pro His Lys Lys Lys Ile Val Arg Thr Glu		
420	425	430
Asp Glu Glu Arg Glu Lys Lys Arg Glu Lys Lys Lys Gln Asp Gln Glu		
435	440	445
Leu Ala Leu Lys Gln Gln Gln Ala Leu Gln Gln Gln Gln Gln Pro		
450	455	460
Pro Gln Pro Pro Gln Gln Ala Pro Ser Lys Gln Asp Gly Thr Ser Thr		
465	470	475
Ser Gln Pro Tyr Val Lys Leu Pro Pro Ala Lys Val Pro Asp Met Asp		
485	490	495
Leu Val Thr Val Ser Leu Val Leu Lys Glu Lys Asn Glu Thr Ile Lys		
500	505	510
Arg Ala Val Leu Glu Lys Leu Arg Lys Arg Lys Glu His Asp Lys Gly		
515	520	525
Phe Ile Asn Leu Thr Asp Asp Pro Tyr Gln Pro Phe Phe Asp Ile Ser		
530	535	540
Thr Asn Arg Ala Glu Glu Leu Ser His Ile Pro Tyr Ser Ser Ile Ala		
545	550	555
Ala Thr His Tyr His Gln Phe Asn Thr Ser Asn Tyr Met Asn Asp Gln		560

565	570	575
Leu Lys Lys Leu Leu Glu Glu Lys Lys Pro Leu Pro Gly Val Lys Thr		
580	585	590
Phe Leu Gly Ser Asn Gly Glu Leu Val Pro Ser Lys Ala Phe Pro His		
595	600	605
Leu Leu Ser Leu Leu Glu Glu Lys Tyr Lys Ala Thr Ser Gly Tyr Ile		
610	615	620
Glu Arg Leu Leu Gln Ser Val Glu Thr Gln Asp Phe Ser Ser Tyr Thr		
625	630	635
Asn Gly Phe Lys Asp Val Glu Pro Lys Glu Thr Asn Glu Pro Val Met		
645	650	655
Ala Phe Pro Gln Arg Ile Arg Arg Val Gly Arg Ala Gly Arg Val		
660	665	670
Phe Leu Asp His Gln Gln Glu Tyr Pro Gln Pro Asn Phe Gln Gln Asp		
675	680	685
Thr Asp Arg Val Gly Gly Ile Pro Asp Val Tyr Cys Lys Glu Asp Ala		
690	695	700
Ile Lys Arg Leu Gln Ser Lys Trp Lys Phe Asp Thr Glu Tyr Lys Thr		
705	710	715
Thr Glu Pro Phe Ser Leu Asp Pro Ser Lys Leu Asn Gly Ile Ser Pro		
725	730	735
Ser Thr Gln Ser Ile Arg Phe Gly Ser Met Leu Leu Asn Arg Thr Arg		
740	745	750
Lys		

<110> 11
<111> 447
<112> DNA
<113> Candida albicans

<120>
<121> CDS
<122> (1)...(447)

<400> 11		
atg tca gat ata gat ata gat aat gta tta aat tta gaa gaa gaa caa		48
Met Ser Asp Ile Asp Ile Asp Asn Val Leu Asn Leu Glu Glu Gln		
1	5	10
		15
tat gaa tta gga ttt aaa gaa ggt caa ata caa gga aca aaa gat caa		
Tyr Glu Leu Gly Phe Lys Glu Gly Gln Ile Gln Gly Thr Lys Asp Gln		96
20	25	30
tat tta gaa gga aaa gaa tat ggt tat caa act gga ttt caa cga ttt		
Tyr Leu Glu Gly Lys Glu Tyr Gly Tyr Gln Thr Gly Phe Gln Arg Phe		144
35	40	45

tta atc att ggt tat att caa gaa tta atg aaa ttt tgg tta tcc cat Leu Ile Ile Gly Tyr Ile Gln Glu Leu Met Lys Phe Trp Leu Ser His	50	55	60	192
ata gat caa tat aat aac tct tct tca ctt cgg aat cat ttg aat aat Ile Asp Gln Tyr Asn Asn Ser Ser Ser Leu Arg Asn His Leu Asn Asn	65	70	75	80
ttg gaa gat att atg gca caa att tct ata acg aat gga gat aaa gaa Leu Gli Asp Ile Met Ala Gln Ile Ser Ile Thr Asn Gly Asp Lys Glu	85	90	95	288
gtt gaa gat tat gaa aaa aat att aaa aag gca aga aat aaa tta aga Val Gli Asp Tyr Glu Lys Asn Ile Lys Lys Ala Arg Asn Lys Leu Arg	100	105	110	336
gtg ata gct aat ata act aaa gaa act tgg aaa att gat tca ttg gat Val Ile Ala Ser Ile Thr Lys Glu Thr Trp Lys Ile Asp Ser Leu Asp	115	120	125	384
aat ttg gtg aaa gaa gta ggt gga act tta caa gti aat gaa aac ccc Asn Leu Val Lys Glu Val Gly Gly Thr Leu Gln Val Ser Glu Asn Pro	130	135	140	432
aat gat gat atg tgg tga Asp Asp Met Trp				447
145				

<110> 12
<111> 148
<112> PRT
<113> Candida albicans

<400> 12

Met Ser Asp Ile Asp Ile Asp Asn Val Leu Asn Leu Glu Glu Gln i	5	10	15
Tyr Glu Leu Gly Phe Lys Glu Gly Gln Ile Gln Gly Thr Lys Asp Gln	20	25	30
Tyr Leu Glu Gly Lys Glu Tyr Gly Tyr Gln Thr Gly Phe Gln Arg Phe	35	40	45
Leu Ile Ile Gly Tyr Ile Gln Glu Leu Met Lys Phe Trp Leu Ser His	50	55	60
Ile Asp Gln Tyr Asn Asn Ser Ser Leu Arg Asn His Leu Asn Asn	65	70	75
Leu Glu Asp Ile Met Ala Gln Ile Ser Ile Thr Asn Gly Asp Lys Glu	85	90	95

Val Glu Asp Tyr Glu Lys Asn Ile Lys Lys Ala Arg Asn Lys Leu Arg
 100 105 110
 Val Ile Ala Ser Ile Thr Lys Glu Thr Trp Lys Ile Asp Ser Leu Asp
 115 120 125
 Asn Leu Val Lys Glu Val Gly Gly Thr Leu Gln Val Ser Glu Asn Pro
 130 135 140
 Asp Asp Met Trp
 145

<210> 13
 <211> 966
 <212> DNA
 <213> Candida albicans

<220>
 <221> CDS
 <222> (1)...(966)

<400> 13

atg ggt aaa aga aga gta gat gaa gaa tct gat tca gat att gat gtt	48
Met Gly Lys Arg Arg Val Asp Glu Glu Ser Asp Ser Asp Ile Asp Val	
1 5 10 15	
agt tca acc gat tca gaa act gaa tta gaa agc aca caa caa caa	96
Ser Ser Thr Asp Ser Glu Thr Glu Leu Glu Ser Thr Gln Gln Gln	
20 25 30	
caa caa caa gaa ggt gct act aca att caa gaa act gtt gat gtt gat	144
Gln Gln Gln Glu Gly Ala Thr Thr Ile Gln Glu Thr Val Asp Val Asp	
35 40 45	
tct gat ttt ttt gat tta aat cct caa att gat ttc cat gct act aag	192
Phe Asp Phe Phe Asp Leu Asn Pro Gln Ile Asp Phe His Ala Thr Lys	
50 55 60	
aat ttt tta aga caa tta ttt ggt gat gat aat gga gaa ttt aat tta	240
Asn Phe Leu Arg Gln Leu Phe Gly Asp Asp Asn Gly Glu Phe Asn Leu	
65 70 75 80	
agt gaa ata gcc gat tta att tta tga gaa aat tcc gtg ggg aca tca	288
Ser Glu Ile Ala Asp Leu Ile Leu Arg Glu Asn Ser Val Gly Thr Ser	
85 90 95	
att aaa act gaa gga atg gaa agt gat cca ttt gca att tta agt gta	336
Ile Lys Thr Glu Gly Met Glu Ser Asp Pro Phe Ala Ile Leu Ser Val	
100 105 110	

att aat tta act aat aat tta aat gtg gcc gtg att aaa caa ttg att Ile Asn Leu Thr Asn Asn Leu Asn Val Ala Val Ile Lys Gln Leu Ile	115	120	125	384
gaa tat att tca aat aaa acc aaa tct aaa act gaa ttc aat att att Glu Tyr Ile Ser Asn Lys Thr Lys Ser Lys Thr Glu Phe Asn Ile Ile	130	135	140	432
ttg aaa aaa ttg tta acc aat cag aac gat act act aga gat agg aaa Leu Lys Lys Leu Leu Thr Asn Gln Asn Asp Thr Thr Arg Asp Arg Lys	145	150	155	480
ttt aaa act gga tta ata att agt gaa aga ttt ata aat atg cca gtt Phe Lys Thr Gly Leu Ile Ile Ser Glu Arg Phe Ile Asn Met Pro Val	165	170	175	528
gaa gtg att cca cca atg tat aaa atg ctt tta caa gaa atg gaa aaa Glu Val Ile Pro Pro Met Tyr Lys Met Leu Leu Gin Glu Met Glu Lys	180	185	190	576
gct gaa gat gct cat gaa aat tat gaa ttt gat tat ttt tta att ata Ala Glu Asp Ala His Glu Asn Tyr Glu Phe Asp Tyr Phe Leu Ile Ile	195	200	205	624
tca aga gtt tat caa tta gtt gat cca gtg gaa aga gaa gat gaa gat Ser Arg Val Tyr Gln Leu Val Asp Pro Val Glu Arg Glu Asp Glu Asp	210	215	220	672
cac gaa aaa gaa tcc aat cgt aaa aag aag aac aag aat aag aag aag His Glu Lys Glu Ser Asn Arg Lys Lys Asn Lys Asn Lys Lys Lys	225	230	235	720
aaa ttg gct aat aat gaa cca aaa cca ata gaa atg gat tat ttc cat Lys Leu Ala Asn Asn Glu Pro Lys Pro Ile Glu Met Asp Tyr Phe His	245	250	255	768
ttt gaa gat caa att ttg gaa tca aat act caa ttt aaa gga ata ttt Leu Glu Asp Gln Ile Leu Glu Ser Asn Thr Gln Phe Lys Gly Ile Phe	260	265	270	816
gaa tat aat aat gaa aat aaa caa gaa aca gat tca aga aga gta ttt Glu Tyr Asn Asn Glu Asn Lys Gln Glu Thr Asp Ser Arg Arg Val Phe	275	280	285	864
act gaa tat ggt att gat ctt aaa tta agt tta acc tta att gat aaa Thr Glu Tyr Gly Ile Asp Pro Lys Leu Ser Leu Ile Leu Ile Asp Lys	290	295	300	912

gat aat tta gct aaa tca gtc att gaa atg gaa caa caa ttc cca cct 960
Asp Asn Leu Ala Lys Ser Val Ile Glu Met Glu Gln Gln Phe Pro Pro
305 310 315 320

tca taa 966
Pro

<210> 14
<211> 321
<212> PRT
<213> Candida albicans

<400> 14
Met Gly Lys Arg Arg Val Asp Glu Glu Ser Asp Ser Asp Ile Asp Val
1 5 10 15
Ser Ser Thr Asp Ser Glu Thr Glu Leu Glu Ser Thr Gln Gln Gln Gln
20 25 30
Gln Gln Glu Gly Ala Thr Thr Ile Gln Glu Thr Val Asp Val Asp
35 40 45
Phe Asp Phe Phe Asp Leu Asn Pro Gln Ile Asp Phe His Ala Thr Lys
50 55 60
Asn Phe Leu Arg Gln Leu Phe Gly Asp Asp Asn Gly Glu Phe Asn Leu
65 70 75 80
Ser Glu Ile Ala Asp Leu Ile Leu Arg Glu Asn Ser Val Gly Thr Ser
85 90 95
Ile Lys Thr Glu Gly Met Glu Ser Asp Pro Phe Ala Ile Leu Ser Val
100 105 110
Ile Asn Leu Thr Asn Asn Leu Asn Val Ala Val Ile Lys Gln Leu Ile
115 120 125
Glu Tyr Ile Ser Asn Lys Thr Lys Ser Lys Thr Glu Phe Asn Ile Ile
130 135 140
Leu Lys Lys Leu Leu Thr Asn Gln Asn Asp Thr Thr Arg Asp Arg Lys
145 150 155 160
Phe Lys Thr Gly Leu Ile Ile Ser Glu Arg Phe Ile Asn Met Pro Val
165 170 175
Glu Val Ile Pro Pro Met Tyr Lys Met Leu Leu Gln Glu Met Glu Lys
180 185 190
Ala Glu Asp Ala His Glu Asn Tyr Glu Phe Asp Tyr Phe Leu Ile Ile
195 200 205
Ser Arg Val Tyr Gln Leu Val Asp Pro Val Glu Arg Glu Asp Glu Asp
210 215 220
His Glu Lys Glu Ser Asn Arg Lys Lys Asn Lys Asn Lys Lys Lys
225 230 235 240
Lys Leu Ala Asn Asn Glu Pro Lys Pro Ile Glu Met Asp Tyr Phe His
245 250 255
Leu Glu Asp Gln Ile Leu Glu Ser Asn Thr Gln Phe Lys Gly Ile Phe

260 265 270
Glu Tyr Asn Asn Glu Asn Lys Gln Glu Thr Asp Ser Arg Arg Val Phe
275 280 285
Thr Glu Tyr Gly Ile Asp Pro Lys Leu Ser Leu Ile Leu Ile Asp Lys
290 295 300
Asp Asn Leu Ala Lys Ser Val Ile Glu Met Glu Gln Gln Phe Pro Pro
305 310 315 320
Pro

<310> 15
<311> 310
<312> DNA
<313> Candida albicans

<400> 15
caatttatcc atggccgtt ctggaaattt gattttggtt aaactgtcaa tgaatttagaa 60
aaatcgcaag atttgcctaa tgaatatatg attgtggaga atgtgccatt attaaataga 120
tttattayta tacctaagga gtatggcgc ttaaattgtt cagcattgt tgccggata 180
attgagggag cacttgatcc tagtggatc aatgccatg ttacagcaca cacggtcgt 240
acagatgraa atccattaag aacagtattt ttgatcaagt ttgacgatcc tggtttaatt 300
agagagatgt tgagatttgg 320

<310> 16
<311> 295
<312> DNA
<313> Candida albicans

<400> 16
gttcatgtt ggtgactcag agcgtctcaa ctatattgtt cgattataca tacgaactcg 60
atggagiaag ttgaataaaat ttactatttt ttacatcaat gaaaggcgc aaaatgataa 120
tttattgtcc aaagagggaaa gagattatac acacaaatat ttccagatcc tgactcaatt 180
atataacaaac tgtttctca aaaaaactacc acaaattgtt acctatttgg atgacaccag 240
ngtgtggaaaa tcaatgatcg ttgagccaga ttttagaccag cctgtgtta tcaaa 295

<310> 17
<311> 392
<312> DNA
<313> Candida albicans

<400> 17
atctctgata tgagatttgg cttaaaaggc gatccaattt aattggcccg agtggggat 60
gcacccaaug atagtttccgc gacataacgt actcaatatgg gactccatca tcattggag 120
accccaatac tggtggatcc tacattgggt gagttggccc atttggccag atcgacttta 180
ggtggacaaa gatgtttggat cattcaaaata tttagggagaa tcctccataa atttggattta 240

cataatataca gtataactacc aaaccagctc aatgatcaga gttttacaga tgaatcaaaa 300
ctatcacttg acsttgaaga tagatgtggg atttgataga ccaattacga atcattgaaa 360
caataacaga gggagctgat ggaaaaaaaga cc 373

<21> 18
<211> 335
<212> DNA
<213> Candida albicans

<400> 18
atcccccaccc cggacgccttc gaggatatgg cccgaggcac acaagtatta caaggatcaa 60
aagttaaagg agccagagac atatatcaag ttttagtgcca cagtagagga cacagtgggt 120
gtggagtgaca atatggacga ggttagatgaa aagttttata gagagacact atgcaagtac 180
tatcccaaaa agaaaaaacaa gtcagatgag aacaatcgaa agtgtactga attggagttt 240
gaaaacaatct gtgacaagtt gaaaaagacc attgaagcac gacaaccgtt tttgtctatg 300
gacccccacca lacatttctatc gtacgaggag ttgtc 335

<210> 19
<211> 326
<212> DNA
<213> Candida albicans

<400> 19
agatatacat aatgtattaa atttagaaga agatcaatat gaattaggat taaaagaagg 60
tcaaatacaa ggaacaaaaag atcaatattt agaaggaaaa gaatatggtt atcaaactgg 120
atttcaacga tttttatca ttggtttat tcaagaattt atgaaatttt gtttatccca 180
tatugatcaa tataataact ttctttcaact tcggaatcat ttgaataatt tggaaagatas 240
tatggcaraa attttatataa cgaatggaga taaaagatgtt gaagattatg aaaaaaatat 300
taaaaaggca agaaataaaat taagag 326

<210> 20
<211> 374
<212> DNA
<213> Candida albicans

<400> 20
ctttaaaatttgg aatttccatgc tactaagaat ttttaagaca ttatgggtg atgataatgg 60
agaatttaat ttaagtgaaa tagccgattt aattttacga gaaaattccg tggggacatc 120
aattaaaaact gaaggaatgg aaagtgtatcc atttgcatt ttaagtgtaa ttaattttaaac 180
taataattttta aatgtggccg tgattaaaca attgattgaa tatattttaa ataaaaaccaa 240
atctaaaaact gaattcaata ttatggaa aaaattgtta accaatcaga acgatactac 300
tagagatagg aaatttaaaa ctggattaat aatttagtgaa agatttataa atatgccagt 360
tgaagtgtatt ccac 374

<210> 21
<211> 35
<212> DNA
<213> *Candida albicans*

<210>
<211> modified_base
<212> (18)
<213> n-a or g or c or t

<400> 21
ttatattttt atgttcgnat ctggaaatg atttt 25

<210> 22
<211> 29
<212> DNA
<213> *Candida albicans*

<400> 22
ccaaatcua aactctctt aattaaaac 29

<210> 23
<211> 38
<212> DNA
<213> *Candida albicans*

<400> 23
gttcatgttt ggtgacttag agcgctctaa cttatattg 38

<210> 24
<211> 33
<212> DNA
<213> *Candida albicans*

<400> 24
tttgataaac acagggttgtt ctaaatctgg ctc 33

<210> 25
<211> 32
<212> DNA
<213> *Candida albicans*

<400> 25
atctctgata tgagatttgg ctttaaggc ga 32

<210> 26
<211> 31
<212> DNA
<213> Candida albicans

<400> 26
gttttttttttccatcagctg cctctgttat tg

32

<210> 7
<211> 30
<212> DNA
<213> Candida albicans

<400> 27
atccccacac cggacgcctc

20

<210> 28
<211> 30
<212> DNA
<213> Candida albicans

<400> 28
gacaactcct cgtacgatag

20

<210> 29
<211> 30
<212> DNA
<213> Candida albicans

<400> 29
agataatgtt ttaaattttag

20

<210> 30
<211> 30
<212> DNA
<213> Candida albicans

<400> 30
atctttttttt atttttttgc

20

<210> 31

<211> 20
<212> DNA
<213> Candida albicans

<400> 31
acctcaaatttg atttccatgc 20

<210> 32
<211> 20
<212> DNA
<213> Candida albicans

<400> 32
gtggaatcac ttcaactggc 20